

OIPe

#2

RAW SEQUENCE LISTING

DATE: 12/04/2001

PATENT APPLICATION: US/09/852,209A / TIME: 13:32:29

Input Set : N:\Crf3\RULE60\09852209A.txt

Output Set: N:\CRF3\12042001\I852209A.raw

5 <110> APPLICANT: ERIKSSON, Ulf
7 AASE, Karin
9 LEE, Xuri
11 PONTEN, Annica
13 UUTELA, Marko
15 ALITALO, Kari
17 OESTMAN, Arne
19 HELDIN, Carl-Henrik
21 BETSHOLTZ, Christer
25 <120> TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
27 THEREFOR, AND USES THEREOF
31 <130> FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
35 <140> CURRENT APPLICATION NUMBER: 09/852,209A
36 <141> CURRENT FILING DATE: 2001-05-10
39 <150> PRIOR APPLICATION NUMBER: 09/410,349
40 <151> PRIOR FILING DATE: 1999-09-30
44 <150> PRIOR APPLICATION NUMBER: 60/110,749
46 <151> PRIOR FILING DATE: 1998-12-03
50 <150> PRIOR APPLICATION NUMBER: 60/113,002
52 <151> PRIOR FILING DATE: 1998-12-18
56 <150> PRIOR APPLICATION NUMBER: 60/135,426
58 <151> PRIOR FILING DATE: 1999-05-21
62 <150> PRIOR APPLICATION NUMBER: 60/144,022
64 <151> PRIOR FILING DATE: 1999-07-15
68 <160> NUMBER OF SEQ ID NOS: 39
72 <170> SOFTWARE: PatentIn Ver. 2.0
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102 <223> OTHER INFORMATION: Can be any amino acid residue
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122 <223> OTHER INFORMATION: Can be any amino acid residue
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192 aaattccagt tttccagcaa caaggaacag aacggagtag aagatcctca gcatgagaga 180
194 attattactg tgtctactaa tggaagtatt cacagcccaa ggtttcctca tacttatcca 240
196 agaaatacgg tcttggtatg gagattagta gcagtagagg aaaatgtatg gatacaactt 300
198 acgtttgatg aaagatttgg gcttgaagac ccagaagatg acatatgcaa gtatgatttt 360
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244 catttagaag aagagaacta cattcatggt ttggaagaga taaacctgaa aagaagagtg 1740
246 gccttatctt cactttatcg ataagtcagt ttatttggtt cattgtgtac atttttatat 1800
248 tctccttttg acattataac tgttggtttt tctaactctg ttaaataatat ctattttttac 1860
250 caaaggtatt taatattott ttttatgaca acttagatca actattttta gcttggtaaa 1920
252 tttttctaaa cacaattggt atagccagag gaacaaagat ggatataaaa atattgttgc 1980
W--> 254 cctggacaaa aatacatgta tntccatccc ggaatggtgc tagagttgga ttaaacctgc 2040
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258 ataattaa                                     2108
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282 20 25 30
286 Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
288 35 40 45
292 Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
294 50 55 60
298 His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
300 65 70 75 80
304 Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
306 85 90 95
310 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
312 100 105 110
316 Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
318 115 120 125
322 Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
324 130 135 140
328 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
330 145 150 155 160
334 Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
336 165 170 175
340 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
342 180 185 190
346 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
348 195 200 205
352 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
354 210 215 220
358 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
360 225 230 235 240
364 Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
366 245 250 255
370 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
372 260 265 270

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376 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
378          275          280          285
382 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
384          290          295          300
388 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
390 305          310          315          320
394 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
396          325          330          335
400 Cys Val Cys Arg Gly Ser Thr Gly Gly
402          340          345
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410 <211> LENGTH: 1536
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414 <213> ORGANISM: Homo sapiens
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424 atccaagaaa tacggtcttg gtatggagat tagtagcagt agaggaaaat gtatggatag 180
426 aacttacgtt tgatgaaaga ttggggcttg aagaccaga agatgacata tgcaagtatg 240
428 attttgtaga agttgaggaa ccagtgatg gaactatatt agggcgctgg tgtggttctg 300
430 gtactgtacc aggaaaacag atttctaaag gaaatcaaat taggataaga tttgtatctg 360
432 atgaatattt tccttctgaa ccagggttct gcatccacta caacattgtc atgccacaat 420
434 tcacagaagc tgtgagtcct tcagtgtctac ccccttcagc tttgccactg gacctgctta 480
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440 ttgttttttg aagaaaatcc agagtgggtg atctgaacct tctaacagag gaggtaagat 660
442 tatacagctg cacacctcgt aacttctcag tgtccataag ggaagaacta aagagaaccg 720
444 ataccatttt ctggccaggt tgtctcctgg ttaaacgctg tggtggggaa tgtgcctgtt 780
446 gtctccacaa ttgcaatgaa tgtcaatgtg tcccaagcaa agttactaaa aaataccacg 840
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460 taaatgttgt attaaataga tcaccagcta gtttcagagt taccatgtac gtattccact 1260
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466 gggcctaaaa tcgtataaaa tctggatttt tttttttttt tttgctcata ttcacatatg 1440
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476 <211> LENGTH: 318
478 <212> TYPE: PRT
480 <213> ORGANISM: Homo sapiens
484 <400> SEQUENCE: 5
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506          50          55          60
510 Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp
512 65          70          75          80
516 Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp
518          85          90          95
522 Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln
524          100          105          110
528 Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly
530          115          120          125
534 Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val
536          130          135          140
540 Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn
542 145          150          155          160
546 Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu
548          165          170          175
552 Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr
554          180          185          190
558 Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val
560          195          200          205
564 Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr
566          210          215          220
570 Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp
572 225          230          235          240
576 Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn
578          245          250          255
582 Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser
584          260          265          270
588 Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr
590          275          280          285
594 Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu His
596          290          295          300
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602 305          310          315
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634 ccgggctggg ctgagccttg gagtcgtcgc ttccccagtg cccgcgcgca gtgagccctc 180

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09852209A.txt

Output Set: N:\CRF3\12042001\I852209A.raw

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L:678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:2584 M:259 W: Allowed number of lines exceeded, <223> Other Information: